

(A)

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      10      20      30      40      50      60      70      80
PbrVIN04  -MDS-----NNTSYIPLPGEEAPSAAVPPPTHRRPEKVFVAVTFSSVIFLLSLVTLIIHQCPGAPRKTVPPEQPDHHRHQ
PbrVIN08  -MDS-----NNTSYIPLPGE-DESAAVPPPTHRRPEKVFVAVTFSSVIFLLSLVTLIIHQCPGAPRKTVPPEQPDHHRHQ
PbrVIN05  -MDTT-----NNTSYAPLPGE-DESAAVHPPTHRRPEKGFVAVTFSSVIFLLSLVTLVINLCGSPPKTVPEQPDHHHQYR
PbrVIN06  -MDTT-----NNTSYAPLPGE-DESAAVHPPTHRRPEKGFVAVTFSSVIFLLSLVTLVINLCGSPPKTVPEQPDHHHQYR
PbrVIN02  -MADPRPFLPSDPDALPYTYTPLNPDEASEIRKROFKELLAVFSG-LLMLSLVVIISGNNSDSHANKNEP----VFL
PbrVIN03  -MADPRPFLPSDPDALPYTYTPLNPDEASEIRKROFKELLAVFSG-LLMLSLVVIISGNNSDSHANKNEP----VFL
PbrVIN01  -MADPRPFLPSDPDALPYTYTPLNPDEASEIRKROFKELLAVFSG-LLMLSLVVIISGNNSDSHANKNEP----VFS
PbrVIN07  -MADPRPFLPSDPDALPYTYTPLNPDEASEIRKROFKELLAVFSG-LLMLSLVVIISGNNSDTHANKNEP----VFL
PbrCWIN01  -MDI-----LRKLAPVFLFASC-VFLITNNNGVEG-----
PbrCWIN02  -MDI-----LRKLAPVFLFASC-VFLITNNNGVEG-----
PbrCWIN03  -MDI-----LRKLAPVFLFASC-VFLITNNNGVEG-----
PbrCWIN04  -MDI-----LRKLAPVFLFASC-VFLITNNNGVEG-----
PbrCWIN05  MMDIT-----AIKLLVEVIFLACCYVFAINNITCVEA-----

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      90      100      110      120      130      140      150      160
PbrVIN04  QPAASTSPEPRSFVSVPGRKLEGVSAKSN--PYFSEASYNWNTNAMESWQRTAFHFQPADNWMN-----
PbrVIN08  QPAASTSPEPRSFVSVPGRKLEGVSAKSN--PYFSEASYNWNTNAMESWQRTAFHFQPADNWMN-----
PbrVIN05  P--ASTSSETRSFVSVPGRKLEGVSAKSY--PHFSEDASYNWNTNAMESWQRTAFHFQPEKNWIN-----
PbrVIN06  P--ASTSSETRSFVSVPGRKLEGVSAKSY--PHFSEDASYNWNTNAMESWQRTAFHFQPEKNWIN-----
PbrVIN02  AKEPYTTRPAKLRPVSRGIAAGVSEKSNRLADAVDGPAPFWNNMSLSWQRTAFHFQPEKNWMN-----
PbrVIN03  AKEPYTTRPAKLRPVSRGIAAGVSEKSNRLADAVDGPAPFWNNMSLSWQRTAFHFQPEKNWMN-----
PbrVIN01  AKEPYTTRPAKLRPVSRGIAAGVSEKSNRLADAVDGPAPFWNNMSLSWQRTAFHFQPEKNWMN-----
PbrVIN07  AKEPYTTRPAKLRPVSRGIAAGVSEKSNRLADAVTGPAPFWNNMSLSWQRTAFHFQPEKNWMNGKLLRGSSAFFTVVCNS
PbrCWIN01  ----SHRIYSRLQNVPAGEVNVQH-----RTAHFQPPKHWIN-----
PbrCWIN02  ----SHRIYSRLQNVPAGEVNVQH-----RTAHFQPPKHWIN-----
PbrCWIN03  ----SHRIYSRLQNVPAGEVNVQH-----RTAHFQPPKHWIN-----
PbrCWIN04  ----SHRIYSRLQNVPAGEVNVQH-----RTAHFQPPKHWIN-----
PbrCWIN05  ----LHNVYPEFQSLAAVKVKQVH-----RTAHFQPPRNWIN-----

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      170      180      190      200      210      220      230      240
PbrVIN04  -----DPNGPLEYKGWYHLFYQYNPD SAVWGNITWGHAVSTDMIHWLYLPLAM
PbrVIN08  -----DPNGPLEYKGWYHLFYQYNPD SAVWGNITWGHAVSTDMIHWLYLPLAM
PbrVIN05  -----DPNGPLEHKGWYHLFYQYNPD SAVWGNITWGHAVSTDMIHWLYLPLAM
PbrVIN06  -----DPNGPLEHKGWYHLFYQYNPD SAVWGNITWGHAVSTDMIHWLYLPLAM
PbrVIN02  -----GPLEYKGWYHFFYQYNPN GAVWGDIVWGHAVSKDLIHWLHPLAM
PbrVIN03  -----GPLEYKGWYHFFYQYNPN GAVWGDIVWGHAVSKDLIHWLHPLAM
PbrVIN01  -----GPLEYKGWYHFFYQYNPN GAVWGDIVWGHAVSKDLIHWLHPLAM
PbrVIN07  IYYSINSYFLFMHGWLQPLMLWLVIPLPAASDPN GPLEYKGWYHFFYQYNPN GATWGDIVWGHAVSKDLIHWLHPLAM
PbrCWIN01  -----GPMFFNGFYHLFYQYNPKGSVWGNIVWAHSVSKDLINWEALPNAT
PbrCWIN02  -----GPMFFNGFYHLFYQYNPKGSVWGNIVWAHSVSKDLINWEALPNAT
PbrCWIN03  -----GPMFFNGFYHLFYQYNPKGSVWGNIVWAHSVSKDLINWEALPNAT
PbrCWIN04  -----APMFFNGFYHLFYQYNPKGSVWGNIVWAHSVSKDLINWEALPNAT
PbrCWIN05  -----GPMYFGGLYHLFYQYNPN GAVWGNIVWAHSVSKDLINWEALPNAT

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      250      260      270      280      290      300      310      320
PbrVIN04  VPDRWFDANGVWTGSATILENGEIMILYTGSTND SVQVQNLAYPANLSDPLLLDWIKYEGNPVLTTPPSGIGSTDFRDPTT
PbrVIN08  VPDRWFDANGVWTGSATILENGDIMILYTGSTND SVQVQTLAYPANLSDPLLLDWIKYEGNPVLTTPPSGIGSTDFRDPTT
PbrVIN05  VPDRWFDANGVWTGSATILEDGOIIMLYTGSTNE SVQVQNLAYPANLSDPLLLDWVKYEGNPILTTPPSGIGSTDFRDPTT
PbrVIN06  VPDRWFDANGVWTGSATILEDGOIIMLYTGSTNE SVQVQNLAYPANLSDPLLLDWVKYEGNPILTTPPSGIGSTDFRDPTT
PbrVIN02  VADQWYDINGVWTGSATILEDGKIIVMLYTGSTNE SVQVQNLAYPADHNDPLLTKWVKYSGNPILVPPP GIGYKDFRDPTT
PbrVIN03  VADQWYDINGVWTGSATILEDGKIIVMLYTGSTNE SVQVQNLAYPADHNDPLLTKWVKYSGNPILVPPP GIGYKDFRDPTT
PbrVIN01  VADQWYDINGVWTGSATILEDGKIIVMLYTGSTNE SVQVQNLAYPADHNDPLLTKWVKYSGNPILVPPP GIGYKDFRDPTT
PbrVIN07  VADQWYDINGVWTGSATILEDGKIIVMLYTGSTNE SVQVQNLAYPADHNDPLLTKWVKYSGNPILVPPP GIGYKDFRDPTT
PbrCWIN01  FPSKSFEDINGTWSGSATILEGNRPPIILYTGLDNDKROIQSYAVPVNISDPYLREWDKPDNDPLVLPSSDMNASQFRDPTT
PbrCWIN02  FPSKSFEDINGTWSGSATILEGNRPPIILYTGLDNDKROIQSYAVPVNISDPYLREWDKPDNDPLVLPSSDMNASQFRDPTT
PbrCWIN03  FPSKSFEDINGTWSGSATILEGNRPPIILYTGLDNDKROIQSYAVPVNISDPYLREWDKPDNDPLVLPSSDMNASQFRDPTT
PbrCWIN04  FPSKSFEDINGTWSGSATILEGNRPPIILYTGLDNDKROIQSYAVPVNISDPYLREWDKPDNDPLVLPSSDMNASQFRDPTT
PbrCWIN05  HPSKPFEDVNGCWSGSATILEGNKPIILYTGLDNDKROIQSYAVPVNISDPYLREWDKPDNDPLVLIPDLGINATAFRDPTT

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	330	340	350	360	370	380	390	400
PbrVIN04	AWIGPD	GKWRITIGSKIN	TGISMVYTTTDFVNYEL	YDGV	LHEVPGTGMWECVDFYPV	SIN	TKGLETSVNNDG	VKHVVK
PbrVIN08	AWIGPD	GKWRITIGSKIN	TGISMVYTTTDFVNYEL	YDGV	LHEVPGTGMWECVDFYPV	SIN	TKGLETSVNNDG	VKHVVK
PbrVIN05	AWIGPD	GKWRITIGSKIN	TGISMVYTTTDFINYL	HDGV	LHEVPGTGMWECVDFYPV	AIN	SGKGLDTSVNSGRIKHVVK	
PbrVIN06	AWIGPD	GKWRITIGSKIN	TGISMVYTTTDFINYL	HDGV	LHEVPGTGMWECVDFYPV	AIN	SGKGLDTSVNSGRIKHVVK	
PbrVIN02	AWYTSQ	GKWRITIGSKIN	KTGISLVYD	TKDFKTYEQLN	GV	LHAVPGTGMWECVDFYPV	SKTSDKGLDTSVNGPDVKHVVK	
PbrVIN03	AWYTSQ	GKWRITIGSKIN	KTGISLVYD	TKDFKTYEQLN	GV	LHAVPGTGMWECVDFYPV	SKTSDKGLDTSVNGPDVKHVVK	
PbrVIN01	AWYTSQ	GKWRITIGSKIN	KTGISLVYD	TKDFKTYEQLN	GV	LHAVPGTGMWECVDFYPV	SKTSDKGLDTSVNGPDVKHVVK	
PbrVIN07	AWYTSE	GKWRITIGSKIN	KTGISLVYD	TKDFKTYEQLN	GV	LHAVPGTGMWECVDFYPV	SKTSDKGLDTSVNGPDVKHVVK	
PbrCWIN01	AWWHN	-GHWRMLVGGKRRKSGMAWLYRSIDFKHWIKAKHPLHSAPLTGMWECPDFFPVALHCKNGLDTSRVGNDVKHVVK						
PbrCWIN02	AWWHN	-GHWRMLVGGKRRKSGMAWLYRSIDFKHWIKAKHPLHSAPLTGMWECPDFFPVALHCKNGLDTSRVGNDVKHVVK						
PbrCWIN03	AWWHN	-GHWRMLVGGKRRKSGMAWLYRSIDFKHWIKAKHPLHSAPLTGMWECPDFFPVALHCKNGLDTSRVGNDVKHVVK						
PbrCWIN04	AWWHN	-GHWRMLVGGKRRKSGMAWLYRSIDFKHWIKAKHPLHSAPLTGMWECPDFFPVALHCKNGLDTSRVGNDVKHVVK						
PbrCWIN05	AWWGN	-GHWRMLVGGKRRKSGMAWLYRSIDFKHWIKAKHPLHSAPLTGMWECPDFFPVALHCKNGLDTSRVGNDVKHVVK						

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	410	420	430	440	450	460	470	480
PbrVIN04	ASLDDTKL	DHYAIGTYFIENETWVPD	PTIDVGIGLRYDYGRY	YASKTFYDQNKERRIL	GWINE	TD	TE	DDLEK
PbrVIN08	ASLDDTKL	DHYAIGTYFIENETWVPD	PTIDVGIGLRYDYGRY	YASKTFYDQNKERRIL	GWINE	TD	TE	DDLEK
PbrVIN05	ASLDDTKL	DHYAIGTYFIENETWVPD	PTIDVGIGLRYDYGRY	YASKTFYDQNKERRIL	GWINE	TD	TE	DDLEK
PbrVIN06	ASLDDTKL	DHYAIGTYFIENETWVPD	PTIDVGIGLRYDYGRY	YASKTFYDQNKERRIL	GWINE	TD	TE	DDLEK
PbrVIN02	ASLDDDRNDYYSLGSYE	EKTGKWWPDNQKIDVGIGLRYDYGIF	YASKTFYDQNKERRIL	GWINE	TD	TE	DDLEK	
PbrVIN03	ASLDDDRNDYYSLGSYE	EKTGKWWPDNQKIDVGIGLRYDYGIF	YASKTFYDQNKERRIL	GWINE	TD	TE	DDLEK	
PbrVIN01	ASLDDDRNDYYSLGSYE	EKTGKWWPDNQKIDVGIGLRYDYGIF	YASKTFYDQNKERRIL	GWINE	TD	TE	DDLEK	
PbrVIN07	ASLDDDRNDYYSLGSYE	EKTGKWWPDNQKIDVGIGLRYDYGIF	YASKTFYDQNKERRIL	GWINE	TD	TE	DDLEK	
PbrCWIN01	VSLDETRYEYYTVGOYEPETE	IYEPDKTSVDGREGLREDYGNFYASKTFDSSKNRRIL	GWANESDS					
PbrCWIN02	VSLDETRYEYYTVGOYEPETE	IYEPDKTSVDGREGLREDYGNFYASKTFDSSKNRRIL	GWANESDS					
PbrCWIN03	VSLDETRYEYYTVGOYEPETE	IYEPDKTSVDGREGLREDYGNFYASKTFDSSKNRRIL	GWANESDS					
PbrCWIN04	VSLDETRYEYYTVGOYEPETE	IYEPDKTSVDGREGLREDYGNFYASKTFDSSKNRRIL	GWANESDS					
PbrCWIN05	VSLDETRYEYYTVGOYEPETE	IYEPDKTSVDGREGLREDYGNFYASKTFDSSKNRRIL	GWANESDS					

↑ Asp239

	490	500	510	520	530	540	550	560
PbrVIN04	QTIPRTVL	FDSKGTGNLLQWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTES-V
PbrVIN08	QTIPRTVL	FDSKGTGNLLQWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTES-V
PbrVIN05	HTIPRTVL	FDSKGTGNLLQWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrVIN06	HTIPRTVL	FDSKGTGNLLQWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrVIN02	QCIPTV	FDDKKTGSNLLQWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrVIN03	QCIPTV	FDDKKTGSNLLQWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrVIN01	QCIPTV	FDDKKTGSNLLQWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrVIN07	QCIPTV	FDDKKTGSNLLQWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrCWIN01	QAIPTLWLD	-PSGQVQLWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrCWIN02	QAIPTLWLD	-PSGQVQLWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrCWIN03	QAIPTLWLD	-PSGQVQLWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrCWIN04	QAIPTLWLD	-PSGQVQLWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV
PbrCWIN05	QAIPTLWLD	-PSGQVQLWPVEE	EELRLNSTEFT-DVLVEAGTIVPLDIGTATQLDIFVDFEIEL					LDTESV

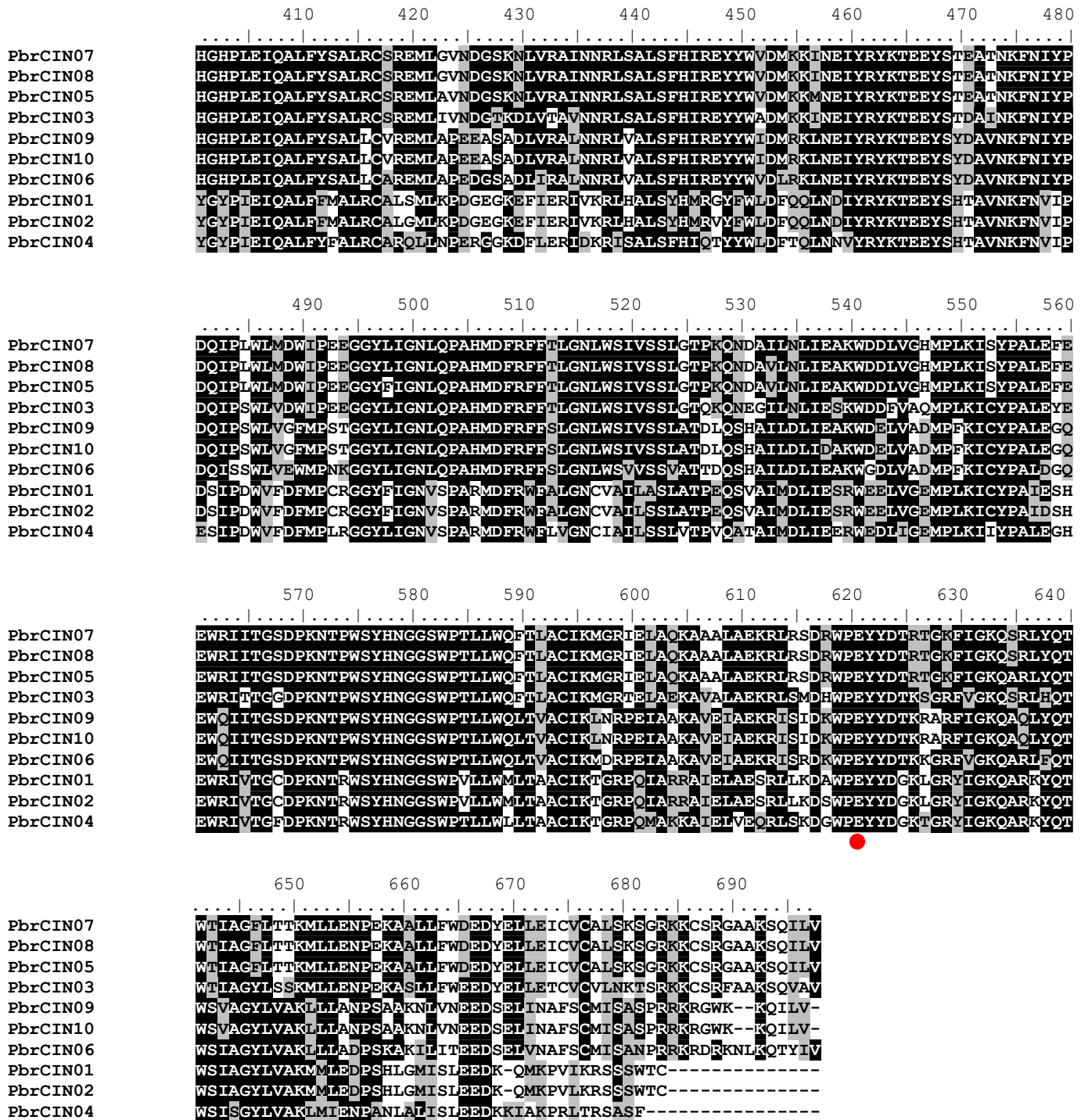
	570	580	590	600	610	620	630	640
PbrVIN04	NGSSGCG	--DGAADRSTFGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV
PbrVIN08	NGSSGCG	--DGAADRSTFGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV
PbrVIN05	NGSSGCG	--DGAADRSTFGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV
PbrVIN06	NGSSGCG	--DGAADRSTFGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV
PbrVIN02	NEVFS	CONTSAGGSHRGALGPFGLLVLADETLSEOTPVYFYVAKGPGGNFDTTFCADQTRSSVANDVKKVVTGS						YV
PbrVIN03	NEVFS	CONTSAGGSHRGALGPFGLLVLADETLSEOTPVYFYVAKGPGGNFDTTFCADQTRSSVANDVKKVVTGS						YV
PbrVIN01	NEVFS	CONTSAGGSHRGALGPFGLLVLADETLSEOTPVYFYVAKGPGGNFDTTFCADQTRSSVANDVKKVVTGS						YV
PbrVIN07	NEMRASWSKLLSNFTSPKDLVAVILITSSAPTKQGR							YV
PbrCWIN01	LDAESV	CALKRNSNPGGVGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV
PbrCWIN02	LDAESV	CALKRNSNPGGVGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV
PbrCWIN03	LDAESV	CALKRNSNPGGVGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV
PbrCWIN04	LDAESV	CALKRNSNPGGVGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV
PbrCWIN05	LDAESV	CALKRNSNPGGVGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSS						EV

	650	660	670	680	690	700	710	720
PbrVIN04	PVLDGETYSARVLVDHSIVESYAQGGRTVISSRVYPT	EAIFYGAARLFLFN	NATGVNVKATLKI	WQLNSAFIHP	PLDQV-			
PbrVIN08	PVLDGETYSARVLVDHSIVESYAQGGRTVISSRVYPT	EAIFYGAARLFLFN	NATGVNVKATLKI	WQLNSAFIHP	PLDQV-			
PbrVIN05	PVLDGETYSARVLVDHSIVESYAQGGRTVISSRVYPT	EAIFYGAARLFLFN	NATGVNVKATLKI	WRLNSAFIHP	PLDQI-			
PbrVIN06	PVLDGETYSARVLVDHSIVESYAQGGRTVISSRVYPT	EAIFYGAARLFLFN	NATGVNVKATLKI	WRLNSAFIHP	PLDQI-			
PbrVIN02	PVLKDEKLSVRILVDHSIVESFAQGGRTTITTRVYPT	KAIYGAARLFLFN	NATEISVTASLKV	WQMNSAFIRPY	HPDETS			
PbrVIN03	PVLKDEKLSVRILVDHSIVESFAQGGRTTITTRVYPT	KAIYGAARLFLFN	NATEISVTASLKV	WQMNSAFIRPY	HPDETS			
PbrVIN01	PVLKDEKLSVRILVDHSIVESFAQGGRTTITTRVYPT	KAIYGAARLFLFN	NATEISVTASLKV	WQMNSAFIRPY	HPDETS			
PbrVIN07	PVLKDEKLSVRILVDHSIVESFAQGGRTTITTRVYPT	KAIYGAARLFLFN	NATEISVTASLKV	WQMNSAFIRPY	HPDETS			
PbrCWIN01	DLAAEKKISLRSLIDHSVVSFAAGGTCILSRVYPTL	AIKDDAOLEVF	NNNGTEPVTVO	TLAAWSMNA	PKQMNQNL	EF--		
PbrCWIN02	DLAAEKKISLRSLIDHSVVSFAAGGTCILSRVYPTL	AIKDDAOLEVF	NNNGTEPVTVO	TLAAWSMNA	PKQMNQNL	EF--		
PbrCWIN03	DLAAEKKISLRSLIDHSVVSFAAGGTCILSRVYPTL	AIKDDAOLEVF	NNNGTEPVTVO	TLAAWSMNA	PKQMNQNL	EF--		
PbrCWIN04	DLAAEKKISLRSLIDHSVVSFAAGGTCILSRVYPTL	AIKDDAOLEVF	NNNGTEPVTVO	TLAAWSMNA	PKQMNQNL	EF--		
PbrCWIN05	DLSHSKKLSLRSLIDHSVVSYGAGGTCITSRVYPTL	AVNNGAHLV	VFNNGTQPVTA	ESLN	AWSMNAP	-TMNKRI----		

	730	740
PbrVIN04	-----	-----
PbrVIN08	-----	-----
PbrVIN05	-----	-----
PbrVIN06	-----	-----
PbrVIN02	NASLNLVTYIKFIVIFFIFLTL	SFLT
PbrVIN03	NASLNLVTYIKFIVIFFIFLTL	SFLT
PbrVIN01	NASSNLVTYIKFIVTFFIFLTF	FIFS-
PbrVIN07	NASFNPFTYIQFIVTFFIFFTL	SFIR
PbrCWIN01	-----	-----
PbrCWIN02	-----	-----
PbrCWIN03	-----	-----
PbrCWIN04	-----	-----
PbrCWIN05	-----	-----

(B)

	10	20	30	40	50	60	70	80
PbrCIN07	-----	MKPTCRILNRR	-----	RNSAFFGFPRPAKWHLGTLTKT	GNSS	SFCVNFEQNSQYHANPERIS	SGPGGVFDDA	
PbrCIN08	-----	MKPTCRILNRR	-----	RNSAFFGFPRPAKWHLGTLTKT	GNSS	SFCVNFEQNSQYHANPERIS	SGPGGVFDDA	
PbrCIN05	-----	MKPTCRILNRC	-----	RNSAFFGFAQPATRLHGLTKT	GNSS	SCCVNFEQNCQYHANPERIS	SGFGGVFDDA	
PbrCIN03		MSSSNCIGICTVSLRPCCRIITGSGYRGSSIFGSGQPK	--LN	RKVTGNLS	----	KLRSRSHDRGCSSQIVRYIRVIDEN		
PbrCIN09	-----	MATSEVVROVMSGELPRMGCE	DI	CLSNMNGVVS	VKPGVKNG	-----	RKISSLSAQVHKSSRVLDR	
PbrCIN10	-----	MATSEVVROVMSGELPRMGCE	DI	CLSNMNGVVS	VKPGVDNG	-----	RKISSLSAQVHKSSRVLDR	
PbrCIN06	-----	MGTFEAVVQVFCGAVPRFC	STDSCFSKCS	PAISSKYHCKCT	-----	KRRVSRDMQMQLLSSGMQOI		
PbrCIN01	-----					MEGT	NEGLRNVSSHCSIS	
PbrCIN02	-----					MEGTKE	GLRNVSSHCSIS	
PbrCIN04	-----	MGKTLNDLLTETKEAEAPPPVPATVEKSSDDVISPERIS	CS	PNDEEEPETKPKSEKSDNSLT	TNEGSTSSLK			
	90	100	110	120	130	140	150	160
PbrCIN07		RKASQVPSWSFGQSGVISRSSRSYSAGIGTTSRGV	--SV	IASLASRFRNLSTSIETRVN	--DNN	FERIYVGGINVKP	--LVE	
PbrCIN08		RKASQVPSWSFGQSGVISRSSRSYSAGIGTTSRGV	--SV	IASLASRFRNLSTSIETRVN	--DNN	FERIYVGGINVKP	--LVE	
PbrCIN05		RKASQVPSWSLQSGGIISR	--SY	SAGVTASRGV	--SV	IASLASRFRNLSTSIETRVN	--DNN	FEEKIYVGGINVKP
PbrCIN03		RRDFSGFDNSNWGRSRVYSANSRVGCRGSSRRRGV	--LV	ILNVASDIRNHSTSVESQVKGKTS	FS	ESIYIQGGLNVKPLVVE		
PbrCIN09		RR--ICVLQG	--RND	VFHGKDRVRRLDS	MSCKCQQA	--ESLTSP	-----	DIDEFKVDQOPNQEAGGFGSNT
PbrCIN10		RR--ICALQG	--RND	VFHGKDRVCRLDS	MSCKCQQP	--ESLTSP	-----	DIDEFKVDQOPNQEAGGFGSNT
PbrCIN06		RTGNYRLNG	--IRS	GLFGKMTVGD	SWILSCKCEQA	--ESIS	GATKDENGTFWVDSTKKFNT	INN
PbrCIN01		DMDDYDL	SRLLDKPR	--LN	IERQSF	DFERSLS	SELSIGLTRVG	----
PbrCIN02		DMDDYDL	SRLLDKPR	--LN	IERQSF	DFERSLS	SELSIGLTRVG	----
PbrCIN04		STEALDYDQIHQMIANWNAESKSKSAESAITSDSSPTEKSS	SEKFTES	LDAGEVPKRKEECERPPAKKT	TNE	QRND	DPV	
	170	180	190	200	210	220	230	240
PbrCIN07		RIDKGE	--NIV	GEEESRI	EVGD	EKKKSES	LINEATVVS	----
PbrCIN08		RIDKGE	--NIV	GEEESRI	EVGD	EKKKSES	LINEATVVS	----
PbrCIN05		RIDKDE	--NIV	REESRI	EVGD	GKKKSES	LINEATVVS	----
PbrCIN03		RIETDRGDVVK	EEESR	VEVNSPNVNVNVN	VNSKGLNDS	KVERELSD	IEE	EA
PbrCIN09		-----	KPTAARKKKGSP	-----	RKSKADI	-----	IEE	EA
PbrCIN10		-----	KPTAARKKKGSP	-----	RKSKADI	-----	IEE	EA
PbrCIN06		-----	IQELKQEK	EGLPNGTNGTVRDAFHKTSIDS	-----	LEDE	AWDL	RES
PbrCIN01		-----				MVAE	AW	EAIRRS
PbrCIN02		-----				MVAE	AW	DALRRS
PbrCIN04			SV	SAAKPGVLLPSP	SVGASLIENLDPWKEGSPKTKS	-----	AGSPGMVE	EAWERL
	250	260	270	280	290	300	310	320
PbrCIN07		ILNYDQVFIRDFVPSALAFLLKGE	GE	-----	IVRN	FLHLTLQ	LSWEKTVDCY	SPGQGLMPASF
PbrCIN08		ILNYDQVFIRDFVPSALAFLLKGE	GE	-----	IVRN	FLHLTLQ	LSWEKTVDCY	SPGQGLMPASF
PbrCIN05		ILNYDQVFIRDFVPSALAFLLKGE	GE	-----	IVRN	FLHLTLQ	LSWEKTVDCY	SPGQGLMPASF
PbrCIN03		PLNYDQVFIRDFVPSALAFLLNGDAE	-----	IVK	NFLHLTLQ	LSWEKTVDCY	SPGQGLMPASF	KVRTVPLDGN
PbrCIN09		TLNYDQVFIRDFIPSGIAFLKGEYD	-----	IVRN	FLHLTLQ	LSWEKTMDCY	SPGQGLMPASF	KVRTVPLDGN
PbrCIN10		TLNYDQVFIRDFIPSGIAFLKGEYD	-----	IVRN	FLHLTLQ	LSWEKTMDCY	SPGQGLMPASF	KVRTVPLDGN
PbrCIN06		TLNYDQVFIRDFIPSGIAFLKGEYD	-----	IVRN	FLHLTLQ	LSWEKTMDCY	SPGQGLMPASF	KVRTVPLDGN
PbrCIN01		VLNYDQVFIRDFVPSALAFLLMNGEPE	-----	IVK	NFLHLTLQ	LSWEKTRIDR	FKLCEG	AMPASF
PbrCIN02		VLNYDQVFIRDFVPSALAFLLMNGEPE	-----	IVK	NFLHLTLQ	LSWEKTRIDR	FKLCEG	AMPASF
PbrCIN04		TLNYNQVFIRDFVPSGLACIMKKEPDQORDVVK	NFLHLTLHLQ	LSWEKTRIDR	FTLCEG	VL	PAS	FKVLF
	330	340	350	360	370	380	390	400
PbrCIN07		DPDFGES	AI	GRVAPVDSGLWWIILLRAYGKITGDYGLQ	ERVDVQTGLK	MILNLCLTDG	FDMFPS	LLVTDG
PbrCIN08		DPDFGES	AI	GRVAPVDSGLWWIILLRAYGKITGDYGLQ	ERVDVQTGLK	MILNLCLTDG	FDMFPS	LLVTDG
PbrCIN05		DPDFGES	AI	GRVAPVDSGLWWIILLRAYGKITGDYGLQ	ERVDVQTGLK	MILNLCLTDG	FDMFPS	LLVTDG
PbrCIN03		DPDFGES	AI	GRVAPVDSGLWWIILLRAYGKITGDYGLQ	ERVDVQTGLK	MILNLCLTDG	FDMFPS	LLVTDG
PbrCIN09		DPDFGE	AI	GRVAPVDSGLWWIILLRAYGKCSRDL	SVQ	ERVDVQTGIK	MILKLCLADG	FDMFPTLLVTDG
PbrCIN10		DPDFGE	AI	GRVAPVDSGLWWIILLRAYGKCSRDL	SVQ	ERVDVQTGIK	MILKLCLADG	FDMFPTLLVTDG
PbrCIN06		DPDFGE	AI	GRVAPVDSGLWWIILLRAYGKCSRDL	SVQ	ERVDVQTGIK	MILKLCLADG	FDMFPTLLVTDG
PbrCIN01		IADFGES	AI	GRVAPVDSGEWWIILLRAYTKSTGDL	SLAETEDCOK	GMRLILSLCL	SEG	FDTFPTLLCADG
PbrCIN02		IADFGES	AI	GRVAPVDSGEWWIILLRAYTKSTGDL	SLAETAD	COK	GMRLILTLCL	SEG
PbrCIN04		VADFGG	SA	IGRVAPVDSGEWWIILLRSYTKCTRDE	SLAELPEVQTGIK	LILNLCLSDG	FDTFPTLLCADG	CSMIDRRMGM



Supplemental Figure S1 Amino acid alignment of CWINs, CINs and VINs in pear. Note, (A) 1: β -fructosidase motif (NDPN) and 2: cysteine catalytic domain (WECV/VD). The triangles present that some members had mutated Asp239, rendering them defective invertase. (B) Amino acid alignment of CINs. Amino acids correspond to active residues for neutral/alkaline invertases were showed by the filled circles, which has been shown to be phosphorylated by calcium-dependent protein kinases (CPK), allowing high-affinity binding with 14-3-3 proteins to increase CIN activities. Black or grey shading corresponds to identical or similar residues, respectively.

Supplemental Table S1 Amino Acid sequences of invertase genes in pear. The incomplete sequences were highlighted by red and excluded in this study.

PbrVIN01(Pbr006369.1)
MADPRPFLPSDPDALPYTYTPLPNPDEASEIRKRQFKELLAVFSGLLMLSLLVVISSGNNSDSHANKNEPVFSAKEPYTTRPAKLRPVSRGIAAGVSEKS
NRLADAVDGPAPFWNNSMLSWQRTAFHFQPEKNWMNGPLFYKGWYHFFYQWNPNGAVWGDIVWGHAVSKDLIHWLHLPLAMVADQWYDINGV
WTGSATILPDGKIVMLYTGSTNESVQVQNLAYPADHNDPLLTKWVKYSGNPILVPPPGVGYKDFRDPTTAWYTSQGKWRITIGSKLNKTGISLVYDTK
DFKTYEQLNGVLHAVPGTGMWECVDFYPVSKTSDKGLDTSVNGPDVKHVVKASLDDDRNDYYSLGSYEETGKWVDPNQKIDVGIGIRYDYGIFYA
SKTFYDQNKERRVLWGWIGESDSENADMQKGWASVQGIPRTVVFDDKKTGSNLLQWPVEEVEKLRLSITDFDKVEVKAGSVLPLQVVTATQLDIVAEF
ELDKKVLESVAESNEVFSCNTSAGGSHRGALGPFGLLVLADETLSEQTPVYFYVAKGPGGNFDTFFCADQTRSSVANDVKKKVTGSYVPVLKDEKLS
VRILVDHSIVESFAQGGRTTITTRVYPTKAIYGAARLFLFNNAATDTSVTASLKVWQMNSAFIRPYHPDETSNASSNLVITYLKFIWTFIFLTFIFS
PbrVIN02(Pbr036856.1)
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NRLADAVDGPAPFWNNSMLSWQRTAFHFQPEKNWMNGPLFYKGWYHFFYQWNPNGAVWGDIVWGHAVSKDLIHWLHLPLAMVADQWYDINGV
WTGSATILPDGKIVMLYTGSTNESVQVQNLAYPADHNDPLLTKWVKYSGNPILVPPPGIGYKDFRDPTTAWYTSQGKWRITIGSKLNKTGISLVYDTK
DFKTYEQLNGVLHAVPGTGMWECVDFYPVSKTSDKGLDTSVNGPDVKHVVKASLDDDRNDYYSLGSYEETGKWVDPNQKIDVGIGIRYDYGIFYA
SKTFYDQNKERRVLWGWIGESDSENADMQKGWASVQGIPRTVVFDDKKTGSNLIQWPVEEVEKLRLSITDFDKVEVKAGSVLPLQVVTATQLDIVAEF
ELDKKVLESVAESNEVFSCNTSAGGSHRGALGPFGLLVLADETLSEQTPVYFYVAKGPGGNFDTFFCADQTRSSVANDVKKKVTGSYVPVLKDEKLS
VRILVDHSIVESFAQGGRTTITTRVYPTKAIYGAARLFLFNNAEISVTASLKVWQMNSAFIRPYHPDETSNASLNLVITYKFIWIFFIFLTLSFLT
PbrVIN03(Pbr036852.1)
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NRLADAVDGPAPFWNNSMLSWQRTAFHFQPEKNWMNGPLFYKGWYHFFYQWNPNGAVWGDIVWGHAVSKDLIHWLHLPLAMVADQWYDINGV
WTGSATILPDGKIVMLYTGSTNESVQVQNLAYPADHNDPLLTKWVKYSGNPILVPPPGIGYKDFRDPTTAWYTSQGKWRITIGSKLNKTGISLVYDTK
DFKTYEQLNGVLHAVPGTGMWECVDFYPVSKTSDKGLDTSVNGPDVKHVVKASLDDDRNDYYSLGSYEETGKWVDPNQKIDVGIGIRYDYGIFYA
SKTFYDQNKERRVLWGWIGESDSENADMQKGWASVQGIPRTVVFDDKKTGSNLIQWPVEEVEKLRLSITDFDKVEVKAGSVLPLQVVTATQLDIVAEF
ELDKKVLESVAESNEVFSCNTSAGGSHRGALGPFGLLVLADETLSEQTPVYFYVAKGPGGNFDTFFCADQTRSSVANDVKKKVTGSYVPVLKDEKLS
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GSATILPNGEIMILYTGSTNDSVQVQNLAYPANLSDPLLLDWIKYEGNPVLTTPSGIGSTDFRDPTTAWIGPDGKWRITIGSKINTTGISMVYTTTTDFVNY
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PbrVIN05(Pbr015752.1)
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PbrVIN06(Pbr012738.1)
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PbrVIN07(Pbr030762.1)
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SATILPNDGIMILYTGSTNDSVQVQTLAYPANLSDPLLLDWIKYEGNPVLTTPSGIGSTDFRDPTTAWIGPDGKWRITIGSKINTTGISMVYTTTTDFVNY
LYDGVLHEVPGTGMWECVDFYPVSINGTKGLETSVNNDGVKHLVKASLDDTKLDHYAIGTYFIENETWVPDDPTIDVGIGLRYDYGRIYASKTFYDQ
NKERRILWGWINETDTETDDLEKGWSSLQTIPTRVLFDSKTGTNLLQWPVEEIEELRLNSTEFTDVLVEAGTTVPLDIGTATQLDIFVDFEIELLDTESVN
GSSGCGDGAADRSTFGPFGILALADETLSELTPVYFRVTNSTDGDVTTYFCADESRSSAPEVFKHVYGGVVPVLDGETYSARVLVDHSIVESYAQGG
TVISSRVYPTKAIYGAARLFLFNNAATGVNVKATLKIWQLNSAFIHPFLDQV

PbrCWIN01(Pbr021809.1)
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LRPF DIKQYRPSFAGYVDVDLAAEKKISLRSLIDHSVVESFAAGGKTCILSRVYPTLAIKDDAQLFVFNNGT EPTVTVQTLAAWSMNAPKQMNQNLEF
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LRPF DIKQYRPSFAGYVDVDLAAEKKISLRSLIDHSVVESFAAGGKTCILSRVYPTLAIKDDAQLFVFNNGT EPTVTVQTLAAWSMNAPKQMNQNLEF
PbrCWIN04(Pbr007632.1)
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GKLIQVKGITAAQADVDTFTLGS LDKAE EFDPNWEK LDAESVCALKRSNPVGGVGPFGLATLASQNLEEF TPVFFRVFKTKENKHKVLMCSDAKSS T
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DRYVPDKELVDGWSGLRYDYGNFYASKTFFDPAKKRRILWGWANESDTASNDAAKGWAGIQITIPRDVWLSPDGKQLLKWPVVELETLRGKKVGIN
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PbrCIN02(Pbr000836.1)
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PbrCIN04(Pbr018376.1)
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PbrCIN06(Pbr028695.1)
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WILLRAYGKCSGDLVQERVDVQTGIKMILRLCLADGDFMFPSSLVTDGSCMIDRRMGIHGHLEIQAIFYSALLCAREMLAPEDGSADLIRALNNRL
VALSFHIREYYWVDLRLKLEIYRYKTEEYSYDAVNKFNIYPDQISSWLVEWMPNKGGLYIGNLQPAHMDFRFFSLGNLWSVSVSVATTDQSHAILDLI
EAKWGDLVADMPFKICYPALDGQEWQIITGSDPKNTPWSYHNGGWSWPTLLWQLTVACIKMDRPEIAAKAVEIAEKIRISDKWPEYYDTHKKGRFVVGKQ
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PbrCIN07(Pbr016455.1)
MKPTCRILNRRRNSAFFGFPRPAKWHLGLTKTGNSSSFCVNFQNSQYHANPFRISGPGGVFDDARKASQVPSWSFGQSGVISRSSRSYSAGIGTTSRGV
SVIASLASRFRNLSTSIETRVNDNNFERIYVQGGINVKPLVERIDKGENIVGEEESRIEVGDEKKSESLNEATVVSPEREYSIDIEKEAWRLLRDSVVMYCG
NPVGTVAANEPGDKQLLNNDQVFIRDFVPSALAFLLKGEGEIVRNFLHLTLQLQSWSEKTVDCYSPGQGLMPASFVKVRTVPLDGNKIEEVLPDFGESAI
GRVAPVDSGLWWIILLRAYGKITGDYGLQERVDVQTGLKMILNLCLTDGDFMFPSSLVTDGSCMIDRRMGIHGHLEIQAIFYSALRCSREMLGVNDG
SKNLVRAINNRLSALSFHIREYYWVDMKKINEIYRYKTEEYSTEATNKFNIPDQIPLWLMDWIPEEGGYLIGNLQPAHMDFRFFTLGNLWSIVSSLGTP
KQNDAILNLIEAKWDDLVGHMPLKISYPALFEFEWRIITGSDPKNTPWSYHNGGWSWPTLLWQFTLACIKMGRIELAQKAAALAEKRLRSDRWPEYYDT
RTGKFIGKQSRLYQWTIAGFLTTKMLLENPEKAALLFWDEDYELLEICVCALSKSGRKKCSRGAAKSQILV

PbrCIN08(Pbr026028.1)
MKPTCRILNRRRNSAFFGFPRPAKWHLGLTKTGNSSSFCVNFQNSQYHANAFRISGPGGVFDDARKASQVPSWSFGQSGVISRSSRSYSAGIGTTSRG
VSVIASLASRFRNLSTSIETRVNDNNFERIYVQGGINVKPLVERIDKGENIVGEEESRIEVGDEKKSESLNEATVVSLEREYSIDIEKEAWRLLRDSVVMYCG
GNPVGTVAANEPGDKQLLNNDQVFIRDFVPSALAFLLKGEGEIVRNFLHLTLQLQSWSEKTVDCYSPGQGLMPASFVKVRTVPLDGNKIEEVLPDFGES
AIGRVAPVDSGLWWIILLRAYGKITGDYGLQERVDVQTGLKMILNLCLTDGDFMFPSSLVTDGSCMIDRRMGIHGHLEIQAIFYSALRCSREMLGVN
DGSKNLVRAINNRLSALSFHIREYYWVDMKKINEIYRYKTEEYSTEATNKFNIPDQIPLWLMDWIPEEGGYLIGNLQPAHMDFRFFTLGNLWSIVSSL
GTPKQNDVAVLNLEIAKWDDLVGHMPLKISYPALFEFEWRIITGSDPKNTPWSYHNGGWSWPTLLWQFTLACIKMGRIELAQKAAALAEKRLRSDRWPE
YYDTRTGKFIGKQSRLYQWTIAGFLTTKMLLENPEKAALLFWDEDYELLEICVCALSKSGRKKCSRGAAKSQILV

PbrCIN09(Pbr004835.1)
MATSEVVRQVMSGELPRMGCFDCLSNMNGVVSVKPGVKNGRKISSLSAQVHKSSRVLRDRRRICVLQGRNDVFHKGDRVRRLDSMSCKCQQAESL
TSPDIDEFKVDQQPNQEAGGFGSNTKPTAARKKKKGSPRKSKADLIEEEAWTLLKNSMVYYCNPVGTIAANDPSSPSTLNNDQVFIRDFIPSGIAFLLKG
EYDIVRNFIHLTLQLQSWSEKTMDCYSPGQGLMPASFVKVRTVPLDGDEFATEDVLPDFGEAAIGRVAPVDSGLWWIILLRAYGKCSRDLVQERVDVQ
TGIMILKLCLADGDFMFPSSLVTDGSCMIDRRMGIHGHLEIQAIFYSALLCVREMLAPEEASADLVRALNNRLVALSFHIREYYWIDMRKLEIYRY
KTEEYSYDAVNKFNIYPDQIPSWLVGFMPSTGGYLIGNLQPAHMDFRFFSLGNLWSIVSSLATDLQSHAILDLIEAKWDELVADMPFKICYPALGQEW
QIITGSDPKNTPWSYHNGGWSWPTLLWQLTVACIKLNRPEIAAKAVEIAEKIRISIDKWPEYYDTKRARFIGKQAQLYQTSVAGYLVAKLLLANPSAAK
NLVNEEDSELINAFSCMISASPRRKRGWKKQILV

PbrCIN10(Pbr003463.1)
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SPDIDEFKVDQQPNQEAGGFGSNTKPTAARKKKKGSPRKSKADLIEEEAWTLLKNSMVYYCNPVGTIAANDPSSPSTLNNDQVFIRDFIPSGIAFLLKG
YDIVRNFIHLTLQLQSWSEKTMDCYSPGGLIPASFVKVRTVPLDGDEFATEDVLPDFGEAAIGRVAPVDSGLWWIILLRAYGKCSRDLVQERVDVQ
GIKMILKLCLADGDFMFPSSLVTDGSCMIDRRMGIHGHLEIQAIFYSALLCVREMLAPEEASADLVRALNNRLVALSFHIREYYWIDMRKLEIYRY
KTEEYSYDAVNKFNIYPDQIPSWLVGFMPSTGGYLIGNLQPAHMDFRFFSLGNLWSIVSSLATDLQSHAILDLIDAKWDELVADMPFKICYPALGQEWQ
IITGSDPKNTPWSYHNGGWSWPTLLWQLTVACIKLNRPEIAAKAVEIAEKIRISIDKWPEYYDTKRARFIGKQAQLYQTSVAGYLVAKLLLANPSAAK
LVNEEDSELINAFSCMISASPRRKRGWKKQILV

Pbr000839.2
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EYSHAAVNKFNVIPDSIPDWVDFMPCRGGYFIGNVSPARMDFRWFALGNCVAILSSLATPEQSVAIMDLIESRWEELVGEMPLKICYPAIDSHEWRIVT
GCDPKNTRWSYHNGGWSWPVLLWMLTAACIKTGRPQIARRAIELAESRLLKDSWPEYYDGKLGRIYIGKQARKYQTSIAGYLVAKMMLEDPSHLGMI
SLEEDKQMKPVLKRSSSWTC

Pbr005836.1
MSPVHADHPSQTGNNTTQETVVFEIGEDSDFLRLLDPRPVSVEKKRSFGRSFSSELSNIGSPCRRSSFGLSPRLNYESHPPVVSDAWETLRRSVVHFRGQ
PVGTLAAVDHSVEELNYDQVFVRDFVPSALAFLMNGEEEEIVKNFLKLTLRLQSLEKIVDQFKLGEVMPASFVVLHDPVRNFETITADFGESAIGRVAP
VDSGFWWIILLRAYTKSTGDTSVSEMEPCQNGIRLILDLCLSEGFDFTXXXXXXXXXXXXXXXXXXXXXXXXXALC

Pbr028541.1
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RCGLYIALMASLLHPSRPGSLIARRAIELAESRLLKDIWPEYCDRWAEHLHPQLRYLVAKMMLENPSHLGMIALEDDKQMKPVMRRSNSWTR

Pbr004247.1
MRAVLLWMLTAACIRTGRPQIARRAIELAESRLLKDAWPEYYDGKLGRIYIGKQARKYQTSIAGYLVAKMMLEDPSHLGMISLQEDKQMKPVIKRSS
SWTC
Pbr005837.1
MGKQARKYQTSIAGYLVAKMMLEDPSHLGMIALEEDQMKPLIKRSASWTS